

1 AAGCTTCGCG GCCTCTGCAG AAGACTTGTG CAAACACTTC CTCTCTGGAC
51 AAGGAGGAAT GCAGGAGGCC ACCGCTGTCA GTACATCTTG GAGTGTGGA
101 GGGATGTGCC TGCACTTGTG AACGGGGGCC AGGAGAATGA GGGCCCAACC
151 AAGCCCGGCA GTGCCAGTA GATGCAGAGA GGCACCCGTG CCCCAGTGA
201 GGGCACAGCC AGTGGGCATC CCTGAGGCCC AGGGGGCCGT TCTCTCCAC
251 TCCCAACAGA TGGCTCTGCT GTGGGGCCCT GGGAGGCCCT TCTCGCCCT
301 GCTTCTGCTG GTTCCATCA AGCAAGTTAC AGGATCGCTC CTCAGGAGA
351 CAACTCAGAA GTGGGCTAAT TATAAGGAGA AGTGTCTGGA AGACTGCCAC
401 AATAGACTTT CTGGCATATT TTGTAATGGG ACATTGTATC GGTATGTGTG
451 CTGGCCCTCAT TCTTATCCTG GAAATGTCTC TGTTCCTGT CTTTCATCT
501 TACCTTGGTG GAATGCAGAG AGCCCAAGGA GGGCTACAG ACACTGCTTG
551 GCTCAGGGGA CTGGCAGAC GCGAGAGAAC ACCACAGATA TTGGCAGGA
601 TGAATCAGAA TGCTCAGAGA ACCACAGCTT CAGACAAAC GTGGATCACT
651 ACGCCTTGCT ATACACCTTG CAGCTGATGT ACACTGTGGG CTACTCCGTG
701 TCTCTCATCT CCGCTCTTCT GGCTCTTACA CTCTCTGTGT TCCTTCGAAA
751 ACTGCATTGC ACACGCAATT ACATCCACAT GAACCTGTTC GCTTCGTCA
801 TCCTGAAAGT TCTGGCTGTC CTGGTGAAGG ACATGTCTCT CCACAACTCT
851 TACTCCAAGA GGGCCGATGA TGAGAGTGGG TGGATGTCTAT ATCTGTCAGA
901 GACATCCGTC TCCTGTCTGT CCGTCCAGGT CCGTCTGCAC TACTTTGTGG
951 GCACCAATCA CTGTGGGCTG CTGGTTGAAG GACTTTACCT CCACACTCTG
1001 CTGGAGCCCA CAGTGTCTCC TGAAGGCGG CTGTGGCCCA AGTACCTGT
1051 GGTGGGTTGG GCCTTCCCA TGTGTTTGT TATTCCTGTG GGTTTGCCC
1101 GTGCACACT GGAGAACACA CGGTCTGGG CCACAAATGG GAACCTGAA
1151 ATCTGTGGA TCATCAGAGG ACCCATGCTG CTTTGTGTA CAGTTAATT
1201 CTTCATCTTC CTCAGATTC TCAAGCTTCT CATTCTAAG CTCAAAGCTC
1251 ATCAGATGTG CTCAGAGAC TACAATACA GATTGGCGAA ATCAAGCTG
1301 CTCCTCATT CTTTGTGGG GGTTCATGAG GTCTCTTCA CTTTCTCCC
1351 CGACGACCAA GTTCAGGAT TTCAAAGC TATTCGACTC TTCATCCAGC
1401 TGACACTGAG CTCTGTCCAC GGATTTCTG TGGCCTTGCA GTATGGCTTT

1451 GCCAATGGAG AGGTGAAGGC AGAGCTGCGA AAGTCATGGG GCCGCTTCTT
 1501 ATTAGCCCGC CACTGGGGCT GCAGAACCTG TGTCTGGGG AAGAATTTC
 1551 GGTTCCTGGG GAAGTGTTC AAGAAGCTGT CGGAGGGAGA TGGCTCTGAG
 1601 ACACTCCAGA AGCTGCGGTT CTCACATGC AGCTCACACC TGGCTCTGAG
 1651 GACCCTGGGA GACGTTGGGG TACAGCCTCA CAGGGGCCGT GGAGCTTGGC
 1701 CCCGGGGAAG CAGCCTGTCT GAGAGCAGTG AGGGAGACTT CACCCTGGCC
 1751 AATACGATGG AGGAGATTCT GGAAGAGAGT GAGATCTAAG GCAGGGTCCA
 1801 TCACCGCAGC TTGGCCACTG ARGAMCCAAC CcTARGAAGG ATKTTGCCGA
 1851 RCCCARGGTC CTCCTCTTCC TATGTWcAT MCCCATTITG ATGTGAAGTC
 1901 TCTCTGGGT GAMCAASCTC TGTACCAACS ARTCTCAGTC CCTCTTGGCC
 1951 TTGTCAcCCT ACTACCCCTC CCCCATCaCa CATgTTTTCC AGAATKTCGG
 2001 TTGGTTTGGG GGGGGGGGTC TTGCCCTAAA TTCAAGTgGA GTGGARCCCA
 2051 CCATGAAGAA AARTCATTTA TTAAATAGAR TCCGGTTAGG ATCTCCTTCC
 2101 CGTTCATGGT GCATGGCCTC CTTCaAGGG ATGGGAGTCG GSTGCACTUG
 2151 AACCCCAAG GAAAcTTTGA AGTATCCAGT TCTAGGGAAT TATAGCCAAT
 2201 ATTCTGAGAG AGCAAGTCTG AGATGAGAC CGAGAATWGC AAGTGTWGA
 2251 CAGCAITCA AGGAaACTCC TCACCTTTgG GCGAAACCTA tGGCAGGATC
 2301 GGCAcGGAGC AGCTATMTG CAAYGCCCGC TCACCTGGGA CATACCACTC
 2351 TCCTTGGCA GSATGTGACC CcATGTGTC CCCAGACTC CTCTCTCCT
 2401 TGCTTSTTT CYTTCCYGT CAAGTCTCAC CTCCTTTCT ACATCTCAGT
 2451 TCWGTITGGT GTYGACAGAA GYTTGAATGT CACAATAGT CATGTGTTAG
 2501 TTTCTGTGCT CATTGCTGTG TCCAATACC TGACCAGGAC CAAITTAAGC
 2551 GAGGAACTC TACATGGGCG GCCGC

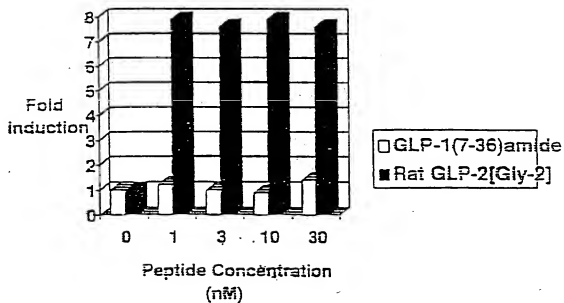
FIGURE 1

09331127.101999

1 MRPQSPAVP SRCREAPVPR VRAQPVGIPE AQQFVPLHSQ QMRLWGPR
51 PFLALLLLVS IKQVTGSLK ETTQKNANYK EKLEDLHNR LSGIFCNGTF
101 DRYVCWPHSY PGNVSVPCPS YLPWNNAESP GRAYRHCLAQ GTWOTRENTT
151 DIWQDESECS ENHSFRQNVD HYALLYTLQL MYTVGYSVSL ISLFLALTLE
201 LFLRLKLECTR NYIHMNLFAS FILKVLAVLV KDMVSHNSYS KRPDESQWM
251 SYLSETSVSC RSQVLLHYF VGTNHLMLLV EGLYLHTLLE PTVFPERRLW
301 PKYLVVGWAF PMLFVIPWGF ARAHLENTRC WATNGNLKIW WIIRGPMLLC
351 VIVNFFIFLK ILKLLISKLK AHQMCFRDYK YRLAKSTLLL IPLLGVEVL
401 FTFFDDQVQ GFSKRIRLFI QLTLSVHGF LVALQYGAN GEVKAELRKS
451 WGRFLARHW GCRTCVLGN FRFLGKCSKK LSEGDSSETL QKLFSTCSCS
501 HLASETLGDV GVQPHRGRGA WPRGSSLSES SEGDFTLANT MEEILEESEI

FIGURE 2

Figure 3

cAMP Response of COS Transfected with Clone

HGLP2 Human GLP-2 Receptor C4-4 vs C9-2R PCR from Clone HMT13

```

1  TCTTCTCTCTC TTATCTCCCTT GTTCTGTGGAT CTCACCTCTCC TGTGTCTTCT
31  TCGAAATCTC CACTGCACGG GCAACTACAT CCACATGAAC TGTGTTGCTT
101  CTTTCATCCT GAGAGACCTG GCTGTACTGG TGAAGGACGT CTTCTCTAC
151  AACTCTTACT CCAAGAGGCC TGACATGAG AATGGGTGGA TGTCTTACT
201  GTCAGAGATG TCCACCTCCT GCGGCTCAGT CCAGGTTCTC TTGCATTACT
251  TTGTGGGTGC CAATTACTTA TGGCTGTGGS TTGAAGGCGT CTACCTCCAC
301  AGGCTGTGTG AGCCACAGT GCTTCTGAG AGGCGGCTGT GCGCCARATA
351  CTTGCTGTTG GGTGSGGCT TCGCTGTGCT ATTTGTTGTA CGGTGGGGTT
401  TCGCCCTGTC ACACCTGGAR AACACAGGCT GCTGGACAC AATGGGAAT
451  AAGAAATCT GTTGGATCAT CCGAGGACCC ATGATGCTCT GTATAACAT
501  CAATTCTTC ATCTTCTGTA AATTCTCAA GCTTCTCATT TCTAAGCTCA
551  AAGCTCATCA AATGTCTTC AGAGATTATA AATACAGATT GCGAAATCA
601  ACACGTGTCC TCACTCTTTT ATGGGCGTT CATGAGATCC TCTTCTTTT
651  CATCACTGAT GATCAG

```

Figure 4

09331127-10199

S F S L I S L F L A L T L L L F L R K L
 T C T T C T C T T A T C T C C T T C T T C T T C T C A G C T C T T T T T T T T T G A A A A C T C
 1 ----- 51

 K C T R A N Y I H M N L F A S F I L R T L
 C A C T G C A G C G C A A C T A C A T C C A C A T G A C T T G T T G C T T C T T C A T C T G A G A A C C T G
 51 ----- 120

 A V L V K D V V T Y N S Y S K R P O N E
 G C T G T A C T G G T G A A G G A C C T C T C T T C A C A C T T A T T A C C A A G A G C C T G A C A A T G A G
 121 ----- 150

 N G W M S Y L S E M S T S C R S V Q V L
 A A T G G G T G G A T G C T A C C T G T C A G A G A T G T C A A C T C C T C C G C T C A C T C C A G G T T C T C
 151 ----- 240

 L N Y F V G A N Y L W L L V E G L Y L H
 T T C A T T A C T T T G T G G T G C C A A T T A C T T A T G S T T G C T T G A G G C C T T A C T T C C A C
 241 ----- 300

 T L L E P T V L P E R A L W P X Y L L L
 A C C T G C T G A G C C C A C A C T G C T T C T G A G A G S T G C T G T G S C T A A T A C C T G C T T T G
 301 ----- 350

 G W A F P V L F V V P W G T A R A H L E
 G G T T G G G C C T C C C T G T G C T A T T T G T T G A C C T G G S T T C G C C C T G C A C A C T G G A A
 351 ----- 420

 N T C C W T T N G N K K I W N I R G P
 A A A C A G S T G C T G G A C A C A A T G G A A T A A A A A A T G T G T G G A T A T C C A G G A G C C
 421 ----- 450

 M N L C V T V N F F I F L N I L N L L I
 A T G A T G C T C T G T A C A C A C T C A A T T C T T C A T E T T C T G A A A T T C T C A G C T T C A T T
 451 ----- 540

 S N L K A H Q M C F R D Y N Y R L A N S
 T T A A G C T C A A A G C T C A C A A A T G C C T C A G A A T T A T A A T A C A G A T G G C A A A T C A
 541 ----- 590

 T L V L I P L L G V H E I L F S F I T D
 A C A C T G T C C T C A T T C T T A T T G G G C G T T C A G A T C C T C T C T T C A T C A C T G A T
 591 ----- 550

 D Q
 G A T C A A G
 551 ----- 557

Figure 5

09:33:127-101999

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(SEQ ID NO: 11)

1 TGGAGAGGATTGTGCAAAACATTCTCTGTGGACCAAGAGGAATGCAAGAGGAGGCTGC 50

 61 CTGCGGTGCATCTTGGACGGCTAGAGAGATGTACCCCTACTTGTGAAGGTGCACGAGGAA 120

 M K L G S S R A G P G R G S A G L L P G
 121 GATGAAGCTGGGATCGAGCAGGCGAGGGCTCTGGAGAGGAAGCGCGGACTCTCTGCTGG 180

 V H E L P M G I P A P W G T S P L S F H
 181 CGTCCAGGACTGGCCATGGGCATCCCTGCCCCCTGGGGGACCACTCTCTCTCTTCCA 240

 R K C S L W A P G R P P L T L L V L L V S
 241 CAGGAAGTGTCTCTCTGGGCCCTCTGGAGGCCCTTCTCTCACTCTGGTCTCTGCTGTTTC 300

 I K Q V T G S L L E E T T R K W A Q V K
 301 CATCAAGCAAGTTACAGGATCCCTCCTTGAGGAACGACTCGGAAGTGGGCTCAGTACAA 360

 Q A C L R D L L K E P S G I F C N G T F
 361 ACAGGCAATGCTGAGAGACTTACTCAAGGAACCTCTGGCATAATTTGTAAACGGGACATT 420

 D Q Y V C W P H S S P G N V S V P C P S
 421 TGATCAGTACGTGTGTGGCCTCATCTTCTCTGGAATGTCTCTGTACCCCTGCCCTTC 480

 Y L P W W S E E S S G R A Y R H C L A Q
 481 ATACTTACCTTGGTGGAGTGAAGAGAGCTCAGGAAGGCCCTACAGACAGTCTGTTGGTCA 540

 G T W Q T I E N A T D I W Q D D S E C S
 541 GGGGACTTGGCAGACGATAGAGAACGCCACGGAATTTGGCAGGATGACTCCGAATGCTC 560

 E N H S F K Q N V D R Y A L L S T L Q L
 601 CGAGAACCACAGCTTCAAGCAAAACGTGGACCGTATGCTTGTCTCAACCTTGCAGCT 660

 M Y T V G Y S F S L I S L F L A L T L L
 661 GATGTACACCGTGGGATCTCTTCTCTCTTATCTCCCTCTCTCTGGCTCTCACCCCTCT 720

 L F L R K L H C T R N Y I H M N L F A S
 721 CTGTGTTCTTGGAAAACCTCACTGCAAGCGCAACTACATCCATGAAGTCTGTTGCTTC 780

 T I L R T L A V L V K D V V F Y N S Y S
 781 TTTCTCTCTGAGAACCTTGGCTGTACTGGTGAAGGACGTGCTCTCTTCAAACTCTTACTC 840

 X R P D N E N G W M S Y L S E M S T S C
 841 CAAGAGGCGCTGACAATGAGATGGGTGGATGCTTACTCTGTCAAGATGTCCACCTCTGT 900

 R S V Q V L L H Y V G A N Y L W L L V
 901 CCGCTCAGTCCAGGTCTCTTGCATTACTTATGGGTGCCAATTACTATGGCTGCTGCT 960

 E G L Y L H T L L E P T V L P E R R L W
 961 TGAAGGCTCTTACTTCCACCGCTGCTGGAGCCCACTGCTCTCTGAGAGGCGGCTGTG 1020

FIGURE 6A

09331127.101999

1021	P R Y L L L G W A F P V L F V V P W G F G C C C A G A T A C C T G C T G T T G G G T T G G G C C T T C C C T G T G C T A T T G T T G T A C C T G G G G T T	1080
1081	A R A H L E N T G C W T T N G N K K I W C G C C G T G C A C A C C T G G A G A A C A C A G G G T G T G G A C A A C A A T G G G A A T A G A A A A T C T G	1140
1141	W I I R G P M M L C V T V N F F I F L K G T G G A T C A T C C G A G G A C C A T G A T G C T C T G T G T A A C A G T C A A T T T C T T C A T C T T C T G A	1200
1201	I L K L L I S K L K A H Q M C F R D Y K A A T T C T C A A G C T T C A T T T C A A G C T C A A G C T C A T C A A A T G T G C T C A G A G A T A T A A	1260
1261	Y R L A K S T L V L I P L L G V H E I L A T A C A G A T T G G C A A A A T C A A C A C T G G T C C T C A T T C C T T A T G G G C G T C A T G A G A T C T	1320
1321	F S F I T D D Q V E G F A K L I R L F I C T T C T C T T C A T C A C T G A T G A T C A A G T T G A A G G A T T G C A A A A C T T A T A G A C A T T T T C A T	1380
1381	Q L T L S S F H G F L V A L Q Y G F A N T C A G T T G A C A C T G A G C T C C T T T C A T G G G T C C T G G G C C T G C A G T A T G T T T G C C A A	1440
1441	G E V K A E L R K Y W V R F L L A R H S T G G A A A G T G A A G G C T G A G C T G C G G A A A T A C T G G G T C C G C T T C T T G C T A G C C G C C A C T C	1500
1501	G C R A C V L G K D F R F L G K C P K K A G G C T G C A G A G C C T G T C C T G G G G A A G G A C T C C G G T C C T A G G A A A A T G T C C C A A G A A	1560
1561	L S E G D G A E K L R K L Q P S L N S G G C T C T C G G A A G G A G A T G C C G C T G A G A A G C T T C G A A G C T G C A G C C T C A C T A A C A G T G G	1620
1621	R L L H L A M R G L G E L G A Q P Q D G C G G C T C T A C A T C T A G C C A T G C G A G G T C T T G G G A G C T G G G C C C A G C C C A A C A G G A	1680
1681	H A R W P R G S S L S E C S E G D V T M C C A T G C A C C T G G C C C G G G C A G C A G C C T G T C C G A G T G C A G T A G G G G S A T G T C A C C A T	1740
1741	A N T M E E I L E E S E I * G G C C A A C A C C A T G G A G G A G A T T C T G G A A G A G A T G A G A T C T A G G G T G A G T T C C A C C A C C	1800
1801	C T G G C T G C T C C A G G S A C T C T T G A G G G G C C A G G A A G A G G A A G C A A G C A G G A C A C A	1860
1861	C G T T G C T G G C A C G S A A T C A T T C G T T C C A T T C A C C A T G C C A C T T T G A T A G A A G C T A	1920
1921	T C A C A A G G T T C T T C A A G C T C T G A T A G A A G C T G T G T G T C A T G C T C A C A G C C T C T G C C	1980
1981	T G C T C T T C T C A T C C T A A T A A C C C C A C C A G T G T G T T T C C A C A A T G C C A C C A G A C C C T A	2040
2041	G G G C C T G C T C T A A A T T C A A G C C A A T G A A G T C C A C C C G G A A T T C T T T G C T T T T A C C C	2100
2101	C T G G A A G A A A T A	2112

FIGURE 6B

Human GLP-2 Receptor Complete Open Reading Frame
 Note: Translation may start with M-1 or M-25.
 Length: 551 April 21, 1997 07:42 Type: P Check: 2775

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1  MKLGSSRAGP GRGSAGLLPG VHSLPMGIPA PMGTSPLSFH RKESLWAFGR
51  PFLTLVLLVS IKQVTGSLLE ETRKWAQYK QACLRDLLKE PSGIFCNGTF
101 DQYVCWPHSS PGNVSVPCPS YLPWNSEESS GRAYRHCLAQ GTWQTENAT
151 DIWQDDSECS ENHSEKQNV DRYALLSTLQL MYTVGYSTSL ISLFLALTLL
201 LFLRKLHCTR NYIHMLFAS FILRTLAVLV ADVVFYNSYS KRPDNENGWM
251 SYLSEMSTSC RSVQVLLHYF VGANYLWLLV EGYLYLSTLLE PTVLPERALW
301 PRYLLLGWAF PVLFPVWPWF ARAHLENTGC WTTNGNKKIW WIIRGPMMLC
351 VTVNFFIFLK ILKLLISXLA AHQMCFRDYK YRLAKSTLVL IPLGVHEIL
401 FSEITDDQVE GFALRLRLFI QLTLSFPHGF LVALQYGFAN GEVXELRKY
451 WVRFLLRKS GCRCACVLGKD RFRLGKCPKX LSEGDGAEXL RKLQPSLNSG
501 RLLHLAMRGL GELGAQPQOD HARWPRGSSL SECSEGDVTM ANTHEEILEE
551 SSI

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FIGURE 7

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666101-211EE60

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PCT/CA97/00969

cAMP Response to GLP-2

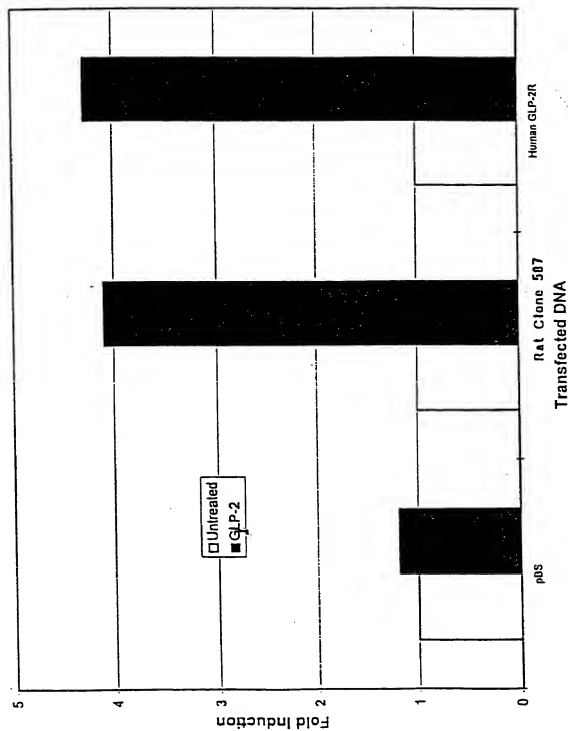


FIGURE 8

1 MRPQSPAPVPSRCREAPVPRVRAQPVGIPEAQGPVPLHSQQMRLWGPGR 50
 1 MKLGSSRAGPGRGSAGLLPGVHELPMGIPAPWGTSPLSFHRKCSLWAPGR 50
 51 PFLALLLLVSIKQVTGSLKETTKWANYKEKCLEDLHNRLSGIFCNGTF 100
 51 PFLTLLVLSIKQVTGSLLEETTRKWAQYKQACLRDLLKEPSGIFCNGTF 100
 101 DRYVCWPHSYPGNVSVPCPSYLPWWNAESPGRAYRHCLAQGTWQTRENTT 150
 101 DQYVCWPHSSPGNVSVPCPSYLPWWSESSGRAYRHCLAQGTWQTIENAT 150
 151 DIWQDESECSSENHSFRQNVDRYHALLYTQLMYTVGYSVSLISLFLALTTF 200
 151 DIWQDSECSSENHSFKQNVDRYALLSTQLMYTVGYSFSLISLFLALTLL 200
 201 LFLRKLHCTRNYIHMNLFASFILKVLAVLVKDMVSHNSYSKRPDDESGWM 250
 201 LFLRKLHCTRNYIHMNLFASFILRTLAVLVKDVVFYNSYSKRPDNENGWM 250
 251 SYLSETSVSCRSVQVLLHYFVGTNHLWLLVEGLYLHTLLEPTVFPERRLW 300
 251 SYLSEMSTSCRSVQVLLHYFVGANYLWLLVEGLYLHTLLEPTVLPERRLW 300
 301 PKYLVVGWAFPMFLFVIPWGFARAHLENTRCWATNGNLKIWWIIRGPMMLC 350
 301 PRYLLLGWAFPVLFVVPWGFARAHLENTGCWTTNGNKKIWWIIRGPMMLC 350
 351 VTVNFFIFLKLKLLISKLAHQMCFRDYKYRLAKSTLLIPLLGVEHL 400
 351 VTVNFFIFLKLKLLISKLAHQMCFRDYKYRLAKSTLVLIPLLGVEHL 400
 401 FTEFPDDQVQGFSKRIRLFIQLTLSSVHGFVALQYGFANGVEKAELRKS 450
 401 FSFITDQVQGFAKLIRLFIQLTLSSFHGFVALQYGFANGVEKAELRKY 450
 451 WGRFLLARHWGCRCTVLGKNFRFLGKCSKLLSEGDSSETLOKRFSTCSS 500
 451 WVRFLLARHSGCRACVLGKDFRFLGKCPKKLSEGDSGAELKRLKQPSLNSG 500
 501 ...HLASETLGDVGVQPHRGAWPRGSSLSSESSEGDFTLANTMEEILEE 547
 501 RLLHLAMRGLGELGAQPQDHRWPRGSSLSESGDVTMANTMEEILEE 550
 548 SEI 550
 551 SEI 553

FIGURE 9

GL2R_RAT_R
HWBRPAT_TR
GLPR_HUMAN

MRPQPSPAVPSRCREAFVPRVRAQFVGIPEAQGFVPLHSQMRLLWGPGR-PFLLALLLV
MCLGSSRAGPGGRSGAGLLPGVHELPMGI PAFWGTISPLSFHRKCSLWAPG-RPFLTLVLV
-----MAGAPGFLRLALLLLGMVGRAGPFP-----
* * *

GL2R_RAT_R
HWBRPAT_TR
GLPR_HUMAN

SIKQVTGSLLETTQKWANYKEKLEDLNRL---SGIFCNGTFRDVRVCPHSPYGP-NVS
SIKQVTGSLLETTQKWANYKEKLEDLNRL---SGIFCNGTFRDVRVCPHSPYGP-NVS
---QGATVSLWETVQKWREYTRQCRSLTEDPPATDLFCNRTFTDETACWPDGEGPSFVN
* * * * *

GL2R_RAT_R
HWBRPAT_TR
GLPR_HUMAN

VPCPSYLPWNNAESPGRAYRHCLAQGTWQTRNTDIDQDESECSNHSFRQNVHDHYALL
VPCPSYLPWNNAESPGRAYRHCLAQGTWQTRNTDIDQDESECSNHSFRQNVHDHYALL
VSCFWYLPWASSVPQGVYTRFCTAEGWLQKDNSSLPLWRDLSECEKRGERSPEEQLL
* * * * *

GL2R_RAT_R
HWBRPAT_TR
GLPR_HUMAN

YTLQLMYTVGVSVSLISLFLALTLFLFLKLECHTRNYIHMNLFASFILKVLAVLVKDMVS
STLQLMYTVGVSVSLISLFLALTLFLFLKLECHTRNYIHMNLFASFILKVLAVLVKDMVS
F-LYIIYTVGYALSFSALVIASAILLGFRLHCHTRNYIHMNLFASFILKVLAVLVKDMVS
* * * * *

GL2R_RAT_R
HWBRPAT_TR
GLPR_HUMAN

HNSYSKRPDDDESQWMSYLS-ETSVSCRSVQVLLHYFVGTNHLWLLVEGLYLHTLLEPTVF
YNSYSKRPDDDESQWMSYLS-ETSVSCRSVQVLLHYFVGTNHLWLLVEGLYLHTLLEPTVF
KMYST-AAQHQWMDGLLSYQDLSCLRVFLMICYVAANTYMLWVEGVLYTLTLAFSVF
* * * * *

GL2R_RAT_R
HWBRPAT_TR
GLPR_HUMAN

PERLWPKYLWVGWAFPMFLVFPWGFARAHLENTRCWATNGNKKIHWIIRGPMMLCVTN
PERLWPKYLWVGWAFPMFLVFPWGFARAHLENTRCWATNGNKKIHWIIRGPMMLCVTN
SEOWIFRLYVSIGWGVPLLVFPWGFARAHLENTRCWATNGNKKIHWIIRGPMMLCVTN
* * * * *

GL2R_RAT_R
HWBRPAT_TR
GLPR_HUMAN

FFIFLKLKLLISLKAHQMCFRDYKIRLAKSTLLLIPLLGVHEVLFTFFDDQVQGFSK
FFIFLKLKLLISLKAHQMCFRDYKIRLAKSTLLLIPLLGVHEVLFTFFDDQVQGFSK
FLIFVRVICIVVSKKANLMCKTDIKRLAKSTLLLIPLLGVHEVLFTFFDDQVQGFSK
* * * * *

GL2R_RAT_R
HWBRPAT_TR
GLPR_HUMAN

RIRLFIOQLTSSVHGFVALQYGFANGEVKAEIRKSWGRFLLARHWGCRCTVLGKNFRFL
RIRLFIOQLTSSVHGFVALQYGFANGEVKAEIRKSWGRFLLARHWGCRCTVLGKNFRFL
FKLFIETLSFTSQGLMVAILYCFVNEVQLEFRKSWERWRLHILHIOQDSMKP-----
* * * * *

GL2R_RAT_R
HWBRPAT_TR
GLPR_HUMAN

GKCSKSLSEGDSSETLQKLRFTSCSS---HLASETLGDVQVPHRGAWPRGSSLSSESS
GKCSKSLSEGDSSETLQKLRFTSCSS---HLASETLGDVQVPHRGAWPRGSSLSSESS
LKCPITSS-LSSGATAGSSMTATCQACSS-----
* * *

GL2R_RAT_R
HWBRPAT_TR
GLPR_HUMAN

EGDFTLANIMEEILEESI
EGDFTLANIMEEILEESI

* * *

FIGURE 10